

Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe

45

```
<210> 6
<211> 15
<212> PRT
<213> Conus atlanticus
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<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8  
 and 13 is Pro or Hy

<400> 6  
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys  
 1 5 10 15

<210> 7  
 <211> 310  
 <212> DNA  
 <213> Conus aurisiacus

<400> 7  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgttt 60  
 gcttctgttt ccccttactg ctcttcgat ggatggagat caatctgtag accgacctga 120  
 agagcgtatg caggacgaca ttcatctga gcagcatccc ttgtttaatc agaaaagaat 180  
 gtgttgccgc gaaggccgga aatgccccag ctatttcaga aacagtcaga tttgtcattg 240  
 ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300  
 cgattgcagt 310

<210> 8  
 <211> 74  
 <212> PRT  
 <213> Conus aurisiacus

<400> 8  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro  
 20 25 30  
 Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe  
 35 40 45  
 Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr  
 50 55 60  
 Phe Arg Asn Ser Gln Ile Cys His Cys Cys  
 65 70

<210> 9  
 <211> 22  
 <212> PRT  
 <213> Conus aurisiacus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i  
 s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,  
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 9  
 Met Cys Cys Gly Xaa Gly Arg Lys Cys Xaa Ser Xaa Phe Arg Asn Ser  
 1 5 10 15  
 Gln Ile Cys His Cys Cys

```
<400> 10
ggatccatga tgtctaaact gggagtccttg ttgaccatct gtttgcttct gtttcccctt 60
actgctcttc cgatcgatgg agatcaatct gtagaccgac ctgcagagcg tatgcaggat 120
gacatttcat ctgagcagca tcgcttggtc aatcagaaaa gaagggtgctg ccggtggcca 180
tgcccccgac aaatcgacgg tgaatattgt ggctgttgcc ttggatgata accgtgttga 240
tgaccaactt tctcgag 257
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<210> 11
<211> 75
<212> PRT
<213> Conus aurisiacus
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<400>      11
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1          5          10          15
Leu Phe Pro Leu Thr Ala Leu Pro Ile Asp Gly Asp Gln Ser Val Asp
20          25          30
Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Arg
35          40          45
Leu Phe Asn Gln Lys Arg Arg Cys Cys Arg Trp Pro Cys Pro Arg Gln
50          55          60
Ile Asp Gly Glu Tyr Cys Gly Cys Cys Leu Gly
65          70          75

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<210> 12
<211> 19
<212> PRT
<213> Conus aurisiacus
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<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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<400> 12
Cys Cys Arg Xaa Xaa Cys Xaa Arg Gln Ile Asp Gly Xaa Xaa Cys Gly
1          5          10          15
Cys Cys Leu

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<210>	13
<211>	262
<212>	DNA
<213>	Conus aurisiacus

<400> 13  
ggatccatga tgtctaaact gggagtccttg ttgaccatct gtctacttct gtttcccctt 60

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<210> 14
<211> 78
<212> PRT
<213> Conus aurisiacus
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Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp  
20 25 30

Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys  
50 55 60

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<210> 15
<211> 23
<212> PRT
<213> Conus aurisiacus
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<220>
<221>  PEPTIDE
<222>  (1)..(23)
<223>  Xaa at residue 1 is Gln or pyro-Glu
```

Lys Asn Leu Lys Cys Cys Ser  
20

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<210> 16
<211> 232
<212> DNA
<213> Conus aurisiacus
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<210> 17
<211> 68
<212> PRT
<213> Conus aurisiacus
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<400>      20
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu
1          5          10          15
Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp
          20          25          30
Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu
          35          40          45
Phe Asp Pro Val Lys Arg Cys Cys Asn Trp Pro Cys Ser Met Gly Cys
          50          55          60

```

```
<210> 21
<211> 16
<212> PRT
<213> Conus bandus
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<400> 21  
Cys Cys Asn Xaa Xaa Cys Ser Met Gly Cys Ile Xaa Cys Cys Xaa Xaa  
1 5 10 15

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<400> 22
caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttctgtct      60
gcttctgttt cccctgactg ctcttcgcgt ggatgaagat caacctgcag accgacctgc      120
agagcgtatg caggacattt catctgaaca gcatcccttg tttgatcccg tcaaacgggtg      180
ttgcgaattg ccatgccatg gatgcgtccc ttgttgctgg ccttaataac gtgtggatga      240
ccaactgtgt tatcacggcc acgtcaagtg tctaataaat aagtaaaatg attgcagt      298
```

<400> 23  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe  
1 5 10 15

Ala Glu Arg Met Gln Asp Ile Ser Ser Glu Gln His Pro Leu Phe Asp  
35 40 45

Cys Trp Pro  
65

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<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 1
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Cys Cys Xaa Leu Xaa Cys His Gly Cys Val Xaa Cys Cys Xaa Xaa  
1 5 10 15

<213> Conus betulinus

caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttctgtct 60

agagcgtatg caggacattt cacctgaaca gcatccctcg tttgatcccg tcaaacggtg 180

ccaactttgt tatcacggcc acgtcaagtg tctgatgaat aagtaaaacg attgcagt 298

<213> Conus betulinus

Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe  
1 5 10 15

Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp  
35 40 45

Pro Val Lys Arg Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys  
50 55 60

<213> Conus betulinus

<223> Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

Cys Cys Gly Leu Xaa Cys Asn Gly Cys Val Xaa Cys Cys Xaa Xaa Ser  
1 5 10 15

<213> Conus betulinus

caagaggggat cgatagcagt tcatgatgtt taaactggga gtcttgttga ccatctatat 60



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<210> 29
<211> 71
<212> PRT
<213> Conus betulinus
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<400>      29
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Tyr Met Leu Leu Phe
1          5          10
Pro Phe Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
          20          25          30
Leu Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Val Asn Pro Trp Phe
          35          40          45
Asp Pro Val Lys Arg Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro
          50          55          60
Cys Cys Pro Asn Trp Pro Ala
65          70

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<210> 30
<211> 18
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 11, 14 and 17 is Pro or Hyp; Xaa at residue 16 is
      Trp or bromo-Tr
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```
<400> 30
Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa Asn Xaa
1          5          10          15
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<210>	31
<211>	325
<212>	DNA
<213>	Conus bullatus

[illegible]

<210> 32

<211> 77  
 <212> PRT  
 <213> Conus bullatus

<400> 32  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu  
 35 40 45  
 Glu Lys Arg Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly  
 50 55 60  
 Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 33  
 <211> 23  
 <212> PRT  
 <213> Conus bullatus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15  
 is Trp or bromo-Tr

<400> 33  
 Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Xaa Cys Gly Arg Xaa Cys  
 1 5 10 15  
 Arg Asp His Ser Arg Cys Cys  
 20

<210> 34  
 <211> 326  
 <212> DNA  
 <213> Conus bullatus

<400> 34  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
 gcttctgttt cccctttttg ctcttcggca ggaaggagat caacctgcag accgacctgc 120  
 agagcgtatg caggatgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg 180  
 tgacaggtgc tgcaaaggga agaggggggtg cggcagatgg tgcagagatc actcacgttg 240  
 ttgcggtcga cgataacgtg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300  
 tagtgattaa gtaaaacgat tgcagt 326

<210> 35  
 <211> 77  
 <212> PRT  
 <213> Conus bullatus

<400> 35  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg

75

 $\langle 220 \rangle$ 

<222> (1) . . (24)

<400> 39

Cys Arg Asp His Ser Arg Cys Cys  
20

<211> 337

<212> DNA

<400> 40

gcttctgttt cccctttttg ctcttccgca ggacggagat caacctgcag accgacctgc 120

agagcgtatg caggacgacc tttcatctga gcagcatccc ttgtttgaga agagaattgt 180

tgacaggtgc tgcaacaaag ggaacgggaa gaggggggtgc agcagatggt gcagagatca 240

ctcacgttgt tgcggtcgac gatgaactgt tqatgaccga ggctttggtt atcacggcta 300

catcaagtgt ctagtgaata agtaaaacga ttgcagt 337

<211> 80

<212> PRT

<213> Conus bullatus

<400> 41

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe  
35 40 45

Glu Lys Arg Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg  
50 55 60

Gly Cys Ser Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
65 70 75 80

<211> 26

<212> PRT

<213> Conus bullatus

 $\langle 220 \rangle$

<221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 18 is Trp or bromo-Trp

<400> 42  
 Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser  
 1 5 10 15  
 Arg Xaa Cys Arg Asp His Ser Arg Cys Cys  
 20 25

<210> 43  
 <211> 337  
 <212> DNA  
 <213> Conus bullatus

<400> 43  
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
 gcttctgttt cccctttttg ctcttcgcga ggatggagat caacctgcag accgacctgc 120  
 tgagcgtatg caggacgaca ttcatctga gcggaatccc ttgtttgaga agagcgttgg 180  
 tttatattgc tgccgacca aacccaacgg gcagatgatg tgcgacagat ggtgcaaaaa 240  
 aaactcacgt tgttgcggtc gacgataatg tgttgatgac cagctttgtt atcaaggcta 300  
 catcaagtat ctagtgaata agtaaaacga ttgcagt 337

<210> 44  
 <211> 77  
 <212> PRT  
 <213> Conus bullatus

<400> 44  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asn Pro Leu Phe Glu Lys  
 35 40 45  
 Ser Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp  
 50 55 60  
 Arg Trp Cys Glu Lys Asn Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 45  
 <211> 27  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 45  
 Val Gly Leu Xaa Cys Cys Arg Xaa Lys Xaa Asn Gly Gln Met Met Cys

1

5

10

15

Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys  
20 25

&lt;210&gt; 46

&lt;211&gt; 323

&lt;212&gt; DNA

&lt;213&gt; Conus bullatus

&lt;400&gt; 46

caagaaggat cgatagcagt tcatgatgtc taaactggga gttttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgtag accgacctgc 120

agaacgtatg caggacgacc tttcatctga gcagcatccc ttgtttgttc agaaaagaag 180

gtgttgccgc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg 240

ttgttaaata acaacgtgtc gatgaccaac ttcggatatca cgactacgcc aagtgtctaa 300

tgaataagta aaacgattgc agt 323

&lt;210&gt; 47

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;400&gt; 47

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe  
35 40 45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr  
50 55 60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys  
65 70

&lt;210&gt; 48

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 48

Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser  
1 5 10 15

Gln Ile Cys Ala Cys Cys  
20

&lt;210&gt; 49

&lt;211&gt; 322

<212> DNA  
 <213> *Conus bullatus*

<400> 49  
 caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60  
 gcttctgttt cccctttttg ctcttccgca ggatggagat caacctgcag accgacctgc 120  
 tgagcgtatg caggacgaca tttcatctga gcaggatccc ttgtttgttc agaaaagaag 180  
 gtgttgccgc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg 240  
 ttgttaaagt acaacgtgtg atgaccaact tcggtatcac gactacgcca agtgtctaata 300  
 gaataagtaa aacgattgca gt 322

<210> 50  
 <211> 74  
 <212> PRT  
 <213> *Conus bullatus*

<400> 50  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asp Pro Leu Phe  
 35 40 45  
 Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr  
 50 55 60  
 Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys  
 65 70

<210> 51  
 <211> 22  
 <212> PRT  
 <213> *Conus bullatus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is  
 s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid  
 ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Ty

<400> 51  
 Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser  
 1 5 10 15  
 Gln Ile Cys Ala Cys Cys  
 20

<210> 52  
 <211> 238  
 <212> DNA  
 <213> *Conus capitaneus*

<400> 52  
 ggatccatga tgtctaaact gggagtcttg gtgaccatct gctgtcttct gtttccccctt 60  
 gctgcttttc cactggatgg aaatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120

gacagttcag ctgccctgat caatacctgg attgatcatt cccattcttg ctgcaggac 180

tgcggtgaag attgtgttg ttgttgccgg taacgtgttg atgaccaact ttctcgag 238

<210> 53

<211> 70

<212> PRT

<213> Conus capitaneus

<400> 53

Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu  
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp  
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn  
35 40 45

Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp  
50 55 60

Cys Val Gly Cys Cys Arg  
65 70

<210> 54

<211> 15

<212> PRT

<213> Conus capitaneus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 8 is Glu or gamma-carboxy Glu

<400> 54

Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg  
1 5 10 15

<210> 55

<211> 323

<212> DNA

<213> Conus characteristicus

<400> 55

caagaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180

gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaagt acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataagta aaatgattgc agt 323

<210> 56

<211> 74

<212> PRT

<213> Conus characteristicus

<400> 56

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100



Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30  
 Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45  
 Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
 50 55 60  
 Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

<210> 57  
 <211> 21  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57  
 Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe  
 1 5 10 15

Ile Cys Gly Cys Cys  
 20

<210> 58  
 <211> 316  
 <212> DNA  
 <213> Conus characteristicus

<400> 58  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60  
 gcttctgttt ccccttactg ctcttcgat ggatggagat gaacctgcaa accgacctgt 120  
 cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180  
 ttgttgact cgcggaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcg 240  
 tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300  
 gtaaaatgat tgcagt 316

<210> 59  
 <211> 75  
 <212> PRT  
 <213> Conus characteristicus

<400> 59  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro  
 20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe



<400> 63  
Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys  
1 5 10 15

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<210> 64
<211> 292
<212> DNA
<213> Conus characteristicus
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```
<210> 65
<211> 69
<212> PRT
<213> Conus characteristicus
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Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys  
50 55 60

```
<210> 66
<211> 15
<212> PRT
<213> Conus characteristicus
```

<400> 66  
Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys

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1              5              10              15
<210> 67
<211> 293
<212> DNA
<213> Conus characteristicus

<400> 67
caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccatctgtct      60
acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc      120
agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgata ccgtcaaacg      180
gtgttgcatg gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataacc      240
tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt          293

<210> 68
<211> 71
<212> PRT
<213> Conus characteristicus

<400> 68
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1              5              10              15
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
                20              25              30
Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
                35              40              45
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50              55              60
Trp Pro Cys Cys Met Phe Gly
65              70

<210> 69
<211> 17
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is
Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 69
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
1              5              10              15
Phe

<210> 70
<211> 232
<212> DNA
<213> Conus characteristicus

<400> 70
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt      60

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<210> 74
<211> 74
<212> PRT
<213> Conus circumcissus
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&lt;400&gt; 74

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45

Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr  
 50 55 60

Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

&lt;210&gt; 75

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus circumciscus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

<223> Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 y

&lt;400&gt; 75

Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

&lt;210&gt; 76

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Conus dalli

&lt;400&gt; 76

caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgata ccgtcaaacg 180

gtgttgcatg gattcggaat gcgactattc ttgctggcct tgctgtattt tatcataacc 240

tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaatgattgc agt 293

&lt;210&gt; 77

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Conus dalli

&lt;400&gt; 77

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45

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Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys  
50 55 60

Trp Pro Cys Cys Ile Leu Ser  
65 70

<210> 78  
<211> 18  
<212> PRT  
<213> Conus dalli

<220>  
<221> PEPTIDE  
<222> (1)..(18)  
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 78  
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile  
1 5 10 15

Leu Ser

<210> 79  
<211> 299  
<212> DNA  
<213> Conus dalli

<400> 79  
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatttgtct 60  
acttctgttt ccccttactg ctgttccact ggatggagat cagcctgcag accgacctgc 120  
agagcgtatg caggacggca tttcatctga acatcatcca ttttttgatt ccgtcaaaaa 180  
gaaacaacag tgttgccgcg cggtggcatg caacatggga tgcgagcctt gttgtggatg 240  
accagctttg ttatcgcggc tcatgaagtg tcctaataa taagtaaaac gattgcagt 299

<210> 80  
<211> 72  
<212> PRT  
<213> Conus dalli

<400> 80  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe  
35 40 45

Asp Ser Val Lys Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn  
50 55 60

Met Gly Cys Glu Pro Cys Cys Gly  
65 70

<210> 81  
<211> 17

<400> 84  
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa  
1 5 10 15



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<400>      88
acctcaagag ggatcgatcg cagttcatga tgtctaaact gggagccttg ttgaccatct      60
gtctgcttct gtttccatt actgctcttc tgatggatgg agatcagcct gcagaccgac      120
ctgcagagcg tacggaggat gacatttcat ctgactacat tccctgttgc agttggccat      180
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gccccgata ctccaacggt aaacttggtt gtttttggtg ccttggtatga taatgtgttg 240  
 atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca 300  
 gta 303

<210> 89  
 <211> 67  
 <212> PRT  
 <213> Conus ermineus

<400> 89  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys  
 35 40 45  
 Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys  
 50 55 60

Cys Leu Gly  
 65

<210> 90  
 <211> 20  
 <212> PRT  
 <213> Conus ermineus

<220>  
 <221> PEPTIDE  
 <222> (1)..(20)  
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or  
 bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 90  
 Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys  
 1 5 10 15

Phe Cys Cys Leu  
 20

<210> 91  
 <211> 241  
 <212> DNA  
 <213> Conus generalis

<400> 91  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60  
 actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120  
 gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180  
 aactttggat gccaaccttg ttgcctcacc tgataacgtg ttgatgacca actttctcga 240  
 g 241

<210> 92  
 <211> 70  
 <212> PRT

<400> 92

<210> 93

$\langle 211 \rangle$	16
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<212> PRT

<213> Conus generalis

<220>

&lt;221&gt; PEPTIDE

<222> (1) .. (16)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or Hy

<400> 93

Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr  
1 5 10 15

<210> 94

$\langle 211 \rangle$     241

<212> DNA

<213> Conus generalis

<400> 94

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa ccctgggtt attgccatca gacagtgttg cacgttctgc 180

aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 95

<211> 70

<212> PRT

<213> Conus generalis

<400> 95

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val  
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp  
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro  
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys

50

55

60

Gln Pro Cys Cys Val Pro  
65 70

<210> 96  
<211> 16  
<212> PRT  
<213> *Conus generalis*

<220>  
<221> PEPTIDE  
<222> (1)..(16)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 96  
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa  
1 5 10 15

<210> 97  
<211> 862  
<212> DNA  
<213> *Conus geographus*

<400> 97  
gtcgactcta gaggatccga caacaaagag tcaacccac tgccacgtca agagcgaagc 60  
gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt 120  
tgaccatctg tctgcttctg tttccctta ctgctcttcc gatggatgga gatgaacctg 180  
caaaccgacc tgtcgagcgt atgcaggaca acatttcac tgagcagtat cccttggttg 240  
agaagagacg agattgttgc actccgccga agaaatgcaa agaccgacaa tgcaaaccac 300  
agagatgttg cgctggacga taacgtgttg atgaccaact ttatcacggc tacgtcaagt 360  
gttttagtgaa taagtaaaat gattgcagtc ttgctcagat ttgcttttgt gtttttgttct 420  
aaagatcaat gaccaaaccg ttgttttgat gcggtattgtc atatatttct cgattccaat 480  
ccaacactag atgatttaat cacgatagat taattttcta tcaatgcctt gatttttctg 540  
ctgtcatatc agttttgttt atattttatt tttcgtcact gtctacacaa acgcatgcat 600  
gcacgcatgc acgcacacac gcacgcacgc tcgcacaaac atgcgcgcgc acgcacacac 660  
acacacacac acacaaacac acacacaagc aatcacacaa ttattgacat tattttattta 720  
ttcattgatg tatttggttat tcgtttgctt gtttttagaa tagtttgagg cgtctttttt 780  
ggatttattt gaactgcttt attgtatacg agtacttctg gctttgaaac actgctgaaa 840  
ataaaacaaa cactgacgta gc 862

<210> 98  
<211> 75  
<212> PRT  
<213> *Conus geographus*

<400> 98  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro  
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg  
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg  
65 70 75

<210> 99  
<211> 22  
<212> PRT  
<213> Conus geographus

<220>  
<221> PEPTIDE  
<222> (1)..(22)  
<223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 99  
Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys  
1 5 10 15

Xaa Gln Arg Cys Cys Ala  
20

<210> 100  
<211> 860  
<212> DNA  
<213> Conus geographus

<400> 100  
ggccagacga caacaaagag tcaacccac tgccacgtca agagcgaagc gccacagcta 60  
agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt tgaccatctg 120  
tgtgcttctg tttccctta ctgctcttcc gatggatgga gatgaacctg caaaccgacc 180  
tgtcgagcgt atgcaggaca acatttcata tgagcagtat cccttgtttg agaagagacg 240  
agattgttgc actccgccga ggaaatgcaa agaccgacga tgcaaacca tgaaatgttg 300  
cgctggacga taacgtgttg atgaccaact ttatcacggc tagctcagtg tttagtgaat 360  
aagtaaaatg attgcagtct tgctcagatt gcttttgtgt tttggtctaa gatcaatgac 420  
caaaccgttg ttttgatgcg gattgtcata tatttctcga ttccaatcca aactagatg 480  
atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt 540  
tttgtttata tttatTTTTT cgtcactgtc tacacaaacg catgcatgca cgcatgcacg 600  
cacacacgca cgcacgctcg cacaacatg cgcgcgcacg cacacacaca cacacacaca 660  
aacacacaca cgaagcaatc acacaattag ttgacattat ttattttatc attgatgtat 720  
ttgttattcg tttgcttggt tttagaatag tttgaggccg tctttttgga tttatttgaa 780  
ctgctttatt gtatacgagt acttcgtgct ttgaaacact gctgaaaata aaacaaacac 840  
tgacgtagca aaaaaaaaaa 860

<210> 101  
 <211> 75  
 <212> PRT  
 <213> Conus geographus

<400> 101  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro  
 20 25 30  
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45  
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg  
 50 55 60  
 Arg Cys Lys Pro Met Lys Cys Cys Ala Gly Arg  
 65 70 75

<210> 102  
 <211> 22  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 102  
 Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys  
 1 5 10 15  
 Xaa Met Lys Cys Cys Ala  
 20

<210> 103  
 <211> 22  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 103  
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys  
 1 5 10 15  
 Xaa Leu Lys Cys Cys Ala  
 20

<210> 104  
 <211> 321  
 <212> DNA  
 <213> Conus gloriamaris

<400> 104  
 ctactatag gaattcgagc tcggtacacg ggatcgatag cagttcatga tgtctaaact 60  
 gggagccttg ttgaccatct gtctacttct gttttcccta actgctgttc cgctggatgg 120

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<210> 105
<211> 71
<212> PRT
<213> Conus gloriamaris
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Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
35 40 45

Trp Pro Cys Cys Met Phe Gly  
65 70

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<210> 106
<211> 17
<212> PRT
<213> Conus gloriamaris
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<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr o
r O-phospho-Ty

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<400> 106  
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met  
1 5 10 15

Phe

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<210> 107
<211> 257
<212> DNA
<213> Conus gloriamaris
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[illegible]

<212> PRT  
<213> Conus gloriamaris

<400> 108  
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe  
1 5 10 15  
Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr  
20 25 30  
Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe  
35 40 45  
Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys  
50 55 60  
Ser Pro Cys Cys Trp  
65

<210> 109  
<211> 17  
<212> PRT  
<213> Conus gloriamaris  
  
<220>  
<221> PEPTIDE  
<222> (1)..(17)  
<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or brom  
o-Tr

<400> 109  
Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys  
1 5 10 15

Xaa

<210> 110  
<211> 471  
<212> DNA  
<213> Conus gloriamaris

<400> 110  
gagacgacaa ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt 60  
gaagaagggt ggagagaggt tcgtgatgtt gaaaatggga gtggtgctat tcattcttctt 120  
ggtactgttt cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc 180  
ggagaacaaa cagctcctca acccagatga aaggagggaa atcatattgc atgctctggg 240  
gacgcgatgc tgttcttggg atgtgtgcga ccacccgagt tgtacttgct gcggcggtta 300  
gcgccgaaca tccatggcgc tgtgctgggc ggttttatcc aacaacgaca gcgtttgttg 360  
atttcatgta tcattgcgcc cacgtctctt gtctaagaat gacgaacatg attgcactct 420  
ggttcagatt tcgtgttctt ttctgacaat aaatgacaaa actccaaaaa a 471

<210> 111  
<211> 71  
<212> PRT  
<213> Conus gloriamaris

<400> 111  
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro



1                      5                      10                      15  
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala  
                     20                      25                      30  
 Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu  
                     35                      40                      45  
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro  
                     50                      55                      60  
 Ser Cys Thr Cys Cys Gly Gly  
                     65                      70

<210> 112  
 <211> 16  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo  
 -Tr

<400> 112  
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly  
 1                      5                      10                      15

<210> 113  
 <211> 304  
 <212> DNA  
 <213> Conus laterculatus

<400> 113  
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60  
 ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccg 120  
 acctgcagag cgtatgcagg acgtttcatc tgaacagcat cccttgatg atcccgtaa 180  
 acggtgttgc gactggccat gcagcggatg catcccttgt tgctaatagt aacaacgtgt 240  
 tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg 300  
 cagt 304

<210> 114  
 <211> 65  
 <212> PRT  
 <213> Conus laterculatus

<400> 114  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1                      5                      10                      15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
                     20                      25                      30  
 Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp  
                     35                      40                      45  
 Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys  
                     50                      55                      60

Cys

65

<210> 115  
 <211> 13  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp

<400> 115  
 Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys  
 1 5 10

<210> 116  
 <211> 313  
 <212> DNA  
 <213> Conus laterculatus

<400> 116  
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60  
 ctgtctgctt ctgtttcccc ttactgctct ggatggagat caacctgcag accgacttgc 120  
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgaaaaga gacgagactg 180  
 ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacgtt gttgcggagg 240  
 ataacgtggt gatgaccaac ttgtttatca cggctacgtc aagtgtctag tgaataagta 300  
 aaacgattgc agt 313

<210> 117  
 <211> 71  
 <212> PRT  
 <213> Conus laterculatus

<400> 117  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu  
 20 25 30  
 Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg  
 35 40 45  
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys  
 50 55 60  
 Pro Ala Arg Cys Cys Gly Gly  
 65 70

<210> 118  
 <211> 22  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 6, 17 and 17 is Pro or Hyp

116  
 313  
 DNA  
 Conus laterculatus

&lt;400&gt; 118

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys  
 1 5 10 15

Xaa Ala Arg Cys Cys Gly  
 20

&lt;210&gt; 119

&lt;211&gt; 314

&lt;212&gt; DNA

&lt;213&gt; Conus laterculatus

&lt;400&gt; 119

gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctgcttc 60  
 tgtttcccct tactgctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc 120  
 gtatgcagga caacatttca tctgagcagc atcacctctt tgaaaagaga cgaccaccat 180  
 gttgcaccta tgacgggagt tgcctaaaag aatcatgcat gcgtaaagct tgttgccgat 240  
 gataacgtgt tgatgaccaa ctttgttctc acggctactc aagtgtctaa tgaataagta 300  
 aaatgattgc agta 314

&lt;210&gt; 120

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Conus laterculatus

&lt;400&gt; 120

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser  
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe  
 35 40 45

Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys  
 50 55 60

Glu Ser Cys Met Arg Lys Ala Cys Cys Gly  
 65 70

&lt;210&gt; 121

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus laterculatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(22)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 121

Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys  
 1 5 10 15

Met Arg Lys Ala Cys Cys  
 20

<210> 122  
 <211> 314  
 <212> DNA  
 <213> Conus laterculatus

<400> 122  
 gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccacc tgtctgcttc 60  
 tgtttccctt tactgctctt ccgatggatg gagatcaact tgcacgccga cctgcagagc 120  
 gtatgcagga caacatttca tctgagcagc atcccttctt tgaaaggaga cgaccaccat 180  
 gttgcaccta tgacgggagt tgccataaag aatcatgcaa gcgtaaagct tgttgcggat 240  
 aataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta 300  
 aaatgattgc agta 314

<210> 123  
 <211> 74  
 <212> PRT  
 <213> Conus laterculatus

<400> 123  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Glu Arg Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys  
 50 55 60  
 Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly  
 65 70

<210> 124  
 <211> 22  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 124  
 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys  
 1 5 10 15  
 Lys Arg Lys Ala Cys Cys  
 20

<210> 125  
 <211> 247  
 <212> DNA  
 <213> Conus leopardus

<400> 125

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60  
 actgctcttc ggctgggttg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120  
 gacattccag atggacagca tccgttaaatt gataggcaga taaactgttg cccgtggcca 180  
 tgccctagta catgccgcca tcaatgctgc cattaatgat aacgtgttga tgaccaactt 240  
 tctcgag 247

<210> 126  
 <211> 71  
 <212> PRT  
 <213> Conus leopardus

<400> 126  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu  
 20 25 30  
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro  
 35 40 45  
 Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr  
 50 55 60  
 Cys Arg His Gln Cys Cys His  
 65 70

<210> 127  
 <211> 19  
 <212> PRT  
 <213> Conus leopardus

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 i  
 s Pro or Hyp; Xaa at residue 7 is Trp or bromo-Tr

<400> 127  
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln  
 1 5 10 15

Cys Cys His

<210> 128  
 <211> 244  
 <212> DNA  
 <213> Conus lividus

<400> 128  
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60  
 actgctcttc ggctgggttag agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120  
 gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttgcca 180  
 tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct 240  
 cgag 244

<210> 129

<211> 71  
 <212> PRT  
 <213> *Conus lividus*

<400> 129  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu  
 20 25 30  
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro  
 35 40 45  
 Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser  
 50 55 60  
 Cys His Tyr Gln Cys Cys His  
 65 70

<210> 130  
 <211> 19  
 <212> PRT  
 <213> *Conus lividus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 130  
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln  
 1 5 10 15

Cys Cys His

<210> 131  
 <211> 275  
 <212> DNA  
 <213> *Conus lynceus*

<400> 131  
 aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat ctgtctgctt 60  
 ctgtttcccc ttactgctct tccgatggat ggagatcaat ctgcagaccg acttgacagag 120  
 cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac 180  
 tgttgacacac ctccgaggaa atgcagagac cgagcctgca aacctcaacg ttgttgcgga 240  
 ggataagctg ttgatgacca actttgttat acggc 275

<210> 132  
 <211> 75  
 <212> PRT  
 <213> *Conus lynceus*

<400> 132  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu

20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45

Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp  
 50 55 60

Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly  
 65 70 75

<210> 133  
 <211> 23  
 <212> PRT  
 <213> Conus lynceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 7, 8 and 18 is Pro or Hyp

<400> 133  
 Gly Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Arg Asp Arg Ala Cys  
 1 5 10 15

Lys Xaa Gln Arg Cys Cys Gly  
 20

<210> 134  
 <211> 803  
 <212> DNA  
 <213> Conus magus

<400> 134  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120  
 cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180  
 ttgttgact cgcgcaaga aatgcaaaga ccgacaatgc aaaccccgaga gatgttgccg 240  
 tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300  
 gtaaaatgat tgcagtcttg ctgagatttg cttttgtgtt ttggtctaaa gatcaatgac 360  
 caaaccgttg ttttgatgcg gattgtcata ttttctcga ttccaatcca aactagatg 420  
 atttaatcac gatagattaa ttttctatca atgccttgat ttttcgtctg tcatatcagt 480  
 tttgtttata tttatTTTTT cgtcactgtc tacacaaacg catgcatgca cgcattgcacg 540  
 cacacacgca cgcacgctcg cacaacatg cgcgcgcacg cacacacaca cacacacaca 600  
 caaacacaca cacgaagcaa tcacacaatt agttgacatt atttatttat tcattgatgt 660  
 atttgttatt cgtttgcttg tttttagaat agtttgaggc ~gtctttttg gatttatttg 720  
 aactgcttta ttgtatacga gtacttcgtg cggggaaaca ctgctgaaaa taaaacaaac 780  
 actgacgtag caaaaaaaaaaaa aaa 803

<210> 135  
 <211> 75  
 <212> PRT

134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999

<400> 135

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro  
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg  
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg  
65 70 75

<210> 136

<211> 22

<212> PRT

<213> Conus magus

 $\langle 220 \rangle$ 

<221> PEPTIDE

<222> (1) .. (22)

<223> Xaa at residue 6 and 7 is Pro or Hyp

<400>	136
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Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys  
1 5 10 15

Xaa Gln Arg Cys Cys Ala  
20

<210> 137

<211> 656

<212> DNA

<213> Conus magus

<400> 137

caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tqagaaaaaaq 180

gtgttgcggc cccggcggtt catgccccgt atatctcaga gacaatttta tttgtggttg 240

ttgttaaattg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatTTTtg gtctaaagat 360

caatgaccaa accgttgttt tgggtgtggat tttcatatat ttctcgaqtc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt tttttatcaa aggcttggtt ttcgtctgt 480

cacatcagtt ttgtttatat ttaatttttc gtcactgatt acacacacgc atgaacgcac 540.

agagtactaa cacatacaca cacacacaca cacacacaca cacacacaca cacacacaca 600

cacacacaca cacgcgcgcg cgcgggcgcca tctagtagcg ccgcqacqac acacac 656

<210> 138

<211> 74

<212> PRT



<400> 138

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys  
65 70

<213> Conus magus

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

Ile Cys Gly Cys Cys  
20

<213> Conus magus

<211> 74

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<400>      141
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1              5              10              15

Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro
              20              25              30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser
              35              40              45

Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr
              50              55              60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys
65              70

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<400> 142
Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
1          5          10          15
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<210>	143
<211>	501
<212>	DNA
<213>	Conus magus

$\langle 210 \rangle$	144
$\langle 211 \rangle$	74
$\langle 212 \rangle$	PRT

<400> 144

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
50 55 60

Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys  
65 70

<210> 145

<211> 23

<212> PRT

<213> Conus magus

 $\langle 220 \rangle$ 

<221> PEPTIDE

<222> (1) .. (23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 145

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Thr Asp  
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
20

<210> 146

<211> 454

<212> DNA

<213> Conus magus

<400> 146

caagaggggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccatctgtct 60

gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca ttatcatctga gcagtatccc ttgtttgata aqaqacaaaa 180

gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaagtg acaacgtgtc gatgaccatc ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtattttg gtctaaagat 360

caatgaccaa accgttgttt tgggtgtggat tttcatatat ttctcgattc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt tttt 454

<210> 147

<211> 74

<212> PRT

<213> Conus magus

<400> 147

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys  
65 70

<210> 148

<211> 23

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P  
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 148

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp  
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
20

<210> 149

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is  
Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 149

Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg  
1 5 10 15

Leu Ile Cys Xaa Cys Cys  
20

<210> 150

<211> 19

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 16 is Pro or Hyp

<400> 150

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa  
1 5 10 15

“T E E N” 00000000

<210>	151
<211>	321
<212>	DNA
<213>	Conus marmoreus
<400>	151

<210>	152
<211>	76
<212>	PRT
<213>	Conus marmoreus

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp  
50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
65 70 75

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<210> 153
<211> 24
<212> PRT
<213> Conus marmoreus
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<223> Xaa at residue 3, 8, 18 and 24 is Pro or Hyp

Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys  
1 5 10 15

<210>	154
<211>	296
<212>	DNA
<213>	Conus marmoreus

gagctcggta ccccgacctc aagagggatc gatagcagtt catgatgtct aaactqqqaa 60

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<210> 155
<211> 68
<212> PRT
<213> Conus marmoreus
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<210> 156
<211> 14
<212> PRT
<213> Conus marmoreus
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<220>
<221>  PEPTIDE
<222>  (1)..(14)
<223>  Xaa at residue 12 is Pro or Hyp
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<210> 157
<211> 355
<212> DNA
<213> Conus marmoreus
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<210>	158
<211>	69
<212>	PRT

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg  
35 40 45





<221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 5 and 7 is Pro or Hyp

<400> 165  
 Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys  
 1 5 10 15

Cys

<210> 166  
 <211> 16  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 6 is Trp or bromo-Trp

<400> 166  
 Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser  
 1 5 10 15

<210> 167  
 <211> 357  
 <212> DNA  
 <213> Conus marmoreus

<400> 167  
 gccaaagcttg catgcctgca ggatgactct agaggatccc cacctcaaga gggatcgata 60  
 gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctacttc tgtttgcct 120  
 tactgctggt cgcctggatg gagatcaacc tgcagaccga cctgcagaac gtatgcagga 180  
 cgacatttca tctgaacgtc atcccatggt tgatgccgtc agagattggt gcccggtgcc 240  
 ggcattgccc tttggatgca acccttggtg tggatgacca gctttgttat cgggacctca 300  
 tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc 357

<210> 168  
 <211> 67  
 <212> PRT  
 <213> Conus marmoreus

<400> 168  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala  
 35 40 45

Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro  
 50 55 60

Cys Cys Gly  
 65

<210> 169  
 <211> 16

<400> 173

Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys  
 1 5 10 15

Val

<210> 174  
 <211> 244  
 <212> DNA  
 <213> Conus nobilis

<400> 174  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60  
 actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120  
 atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180  
 gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240  
 cgag 244

<210> 175  
 <211> 69  
 <212> PRT  
 <213> Conus nobilis

<400> 175  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His  
 20 25 30  
 Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe  
 35 40 45  
 Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe  
 50 55 60

Cys Val Pro Cys Cys  
 65

<210> 176  
 <211> 15  
 <212> PRT  
 <213> Conus nobilis

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8  
 adn 13 is Pro or Hy

<400> 176  
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys  
 1 5 10 15

<210> 177  
 <211> 262  
 <212> DNA  
 <213> Conus nobilis

<400> 177  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

174  
 69  
 175  
 15  
 176  
 177  
 262

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120  
 gacatttcat ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggaag 180  
 aaggggtcat gtcctggcaa agcatgcaaa aatctcaa atgtgtcttg acgataacgt 240  
 gttgatgacc aactttctcg ag 262

<210> 178  
 <211> 78  
 <212> PRT  
 <213> Conus nobilis

<400> 178  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp  
 20 25 30  
 Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro  
 35 40 45  
 Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys  
 50 55 60  
 Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

<210> 179  
 <211> 23  
 <212> PRT  
 <213> Conus nobilis

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 179  
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15  
 Lys Asn Leu Lys Cys Cys Ser  
 20

<210> 180  
 <211> 238  
 <212> DNA  
 <213> Conus pulicarius

<400> 180  
 ggatccatga tgtctaaact gggagtgttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttctttgat cccgtcaaac ggtgttgcaa cagctgttac 180  
 atgggatgca tcccttggtg cttctagtaa taacgtgttg atgaccaact ttctcgag 238

<210> 181  
 <211> 68  
 <212> PRT  
 <213> Conus pulicarius

&lt;400&gt; 181

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp  
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe  
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile  
50 55 60

Pro Cys Cys Phe  
65

&lt;210&gt; 182

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(14)

&lt;223&gt; Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 182

Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
1 5 10

&lt;210&gt; 183

&lt;211&gt; 238

&lt;212&gt; DNA

&lt;213&gt; Conus quercinus

&lt;400&gt; 183

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

acagctcttc agctggatgg agatcaacct gcagaccgac ctgcagagcg tacgcaggac 120

attgcatctg aacagtatcg aaagtttgat cagagacaga ggtgttgcca gtggccatgc 180

cccggtagtt gcagatgctg ccgtactggt taacgtgttg atgaccaact ttctcgag 238

&lt;210&gt; 184

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Conus quercinus

&lt;400&gt; 184

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp  
20 25 30

Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys  
35 40 45

Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys  
50 55 60

Arg Cys Cys Arg Thr Gly  
65 70

181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

<210> 185  
 <211> 17  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr  
 o or Hyp; Xaa at residue 6 is Trp or bromo-Tr

<400> 185  
 Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg  
 1 5 10 15

Thr

<210> 186  
 <211> 15  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 186  
 Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn  
 1 5 10 15

<210> 187  
 <211> 15  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or br  
 omo-Tr

<400> 187  
 Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn  
 1 5 10 15

<210> 188  
 <211> 323  
 <212> DNA  
 <213> Conus radiatus

<400> 188  
 tcaagaagga tcgatagcag ttcgatgatgt ctaaactggg agtcttggtg accatctgtc 60  
 tgcttctggt tccccttact gctcttccga tggatggaga tcaacctgta gaccgacttg 120  
 cagagcgtat gcaggacaac atttcatctg agcag .cac cttctttgaa aagagactac 180  
 catcgtggtg ctcccttaac ttgcggcttt gccagtagc agcatgcaaa cgtaaccctt 240  
 gttgcacagg ataacgtggt gatgaccaac tttgttatca cggctacgtc aagtgtctag 300  
 tgaataagta aaacgattgc agt 323

<210> 189  
 <211> 76  
 <212> PRT  
 <213> Conus radiatus

<400> 189  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Val Asp Arg Leu  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Thr Phe Phe  
 35 40 45  
 Glu Lys Arg Leu Pro Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Pro  
 50 55 60  
 Val Pro Ala Cys Lys Arg Asn Pro Cys Cys Thr Gly  
 65 70 75

<210> 190  
 <211> 24  
 <212> PRT  
 <213> Conus radiatus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp

<400> 190  
 Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala  
 1 5 10 15  
 Cys Lys Arg Asn Xaa Cys Cys Thr  
 20

<210> 191  
 <211> 336  
 <212> DNA  
 <213> Conus radiatus

<400> 191  
 aggtcgactc tagaggatcc ccaaggatcg atagcagttc atgatgtcta aactgggagt 60  
 cttgttgacc atctgtctgc ttctgtttcc ccttactgct cttccgatgg atggagatca 120  
 acctgcagac cgacttgacg agcgtatgca ggacgacatt tcatctgagc agcatccctt 180  
 ctttaaaaag agacaacaaa gatgttgacg cgtaagagg atttgtccag taccagcatg 240  
 cagaagtaaa ccttggtgca aatcataacg tattgatgac caactttggt atcacggcta 300  
 cgtcaagtgt ctagtgaata agtaaaatga ttgcag 336

<210> 192  
 <211> 75  
 <212> PRT  
 <213> Conus radiatus

<400> 192  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe  
35 40 45

Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val  
50 55 60

Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser  
65 70 75

<210> 193

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20  
is Pro or Hy

<400> 193

Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys  
1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser  
20

<210> 194

<211> 326

<212> DNA

<213> Conus radiatus

<400> 194

acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct 60

gtctgcttct gtttcccgtt actgctcttc cgatggatgg tgatcaacct gcagaccgac 120

ttgtagagcg tatgcaggac aacatttcac ctgagcagca tcccttcttt gaaaagagaa 180

gaggaggctg ttgcacacct ccgaggaaat gcaaagaccg agcctgcaaa cctgcacggt 240

gctgcggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc 300

tagtgaataa gtaaaacgat tgcagt 326

<210> 195

<211> 76

<212> PRT

<213> Conus radiatus

<400> 195

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp  
50 55 60



Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
65 70 75

<210> 196  
<211> 24  
<212> PRT  
<213> Conus radiatus

<220>  
<221> PEPTIDE  
<222> (1)..(24)  
<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 196  
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys  
1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa  
20

<210> 197  
<211> 238  
<212> DNA  
<213> Conus rattus

<400> 197  
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gttccctctt 60  
gctgcttttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120  
gacagttcag ctgccctgat caatgcctgg cttgatgaat cccagacttg ctgcagtaac 180  
tgcggtgaag attgtgatgg ttgttgccag taacgtgttg atgaccaact ttctcgag 238

<210> 198  
<211> 70  
<212> PRT  
<213> Conus rattus

<400> 198  
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu  
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp  
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn  
35 40 45

Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp  
50 55 60

Cys Asp Gly Cys Cys Gln  
65 70

<210> 199  
<211> 16  
<212> PRT  
<213> Conus rattus

<220>  
<221> PEPTIDE  
<222> (1)..(16)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or gamma-carboxy Gl

196  
238  
70  
198  
16  
199

&lt;400&gt; 199

Xaa Thr Cys Cys Ser Asn Cys Gly Xaa Asp Cys Asp Gly Cys Cys Gln  
 1 5 10 15

&lt;210&gt; 200

&lt;211&gt; 327

&lt;212&gt; DNA

&lt;213&gt; Conus stercusmuscarum

&lt;400&gt; 200

gacctcaaga gggatcgata gcagttcgtg atgtctaaac tgggagtctt gttgaccatc 60

tgtctgcttc tgtttcctct tactgctctt ccgatggatg gagatcaacc tgcagaccaa 120

cctgcagatc gtatgcagga cgacatttca tctgagcagt atcccttggt tgataagaga 180

caaaagtgtt gcaactgggaa gaaggggtca tgctccggca aagcatgcaa aaatctcaaa 240

tgttgctctg gacgataacg tgttgatgac caactttggt atcacggcta cgtcaagtgt 300

ctaatgaata agtaaaaacga ttgcagt 327

&lt;210&gt; 201

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus stercusmuscarum

&lt;400&gt; 201

Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
 1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala  
 20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp  
 35 40 45

Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys  
 50 55 60

Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

&lt;210&gt; 202

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus stercusmuscarum

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

&lt;223&gt; Xaa at residue 1 is Gln or pyro-Glu

&lt;400&gt; 202

Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
 20

&lt;210&gt; 203

&lt;211&gt; 316

&lt;212&gt; DNA

&lt;213&gt; Conus stercusmuscarum

1000 900 800 700 600 500 400 300 200 100 0

<400> 203  
 gatcgatagc agttcgtgat gtctaaactg ggagtcttgt tgaccatctg tctgcttctg 60  
 tttcccttta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt 120  
 atgcagaacg acatttcatac tgagcagtat cccttgtttg ataagagaca aaagtgttgc 180  
 ggccccggcg cgtcatgccc cagatatttc aaagacaatt ttatttggtg ttgttgtaa 240  
 atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaaagtgc taatgaataa 300  
 gtaaaacgat tgcagt 316  
 <210> 204  
 <211> 73  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 204  
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
 1 5 10 15  
 Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala  
 20 25 30  
 Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp  
 35 40 45  
 Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe  
 50 55 60  
 Lys Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

<210> 205  
 <211> 23  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P  
 ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 205  
 Xaa Lys Cys Cys Gly Xaa Gly Ala Ser Cys Xaa Arg Xaa Phe Lys Asp  
 1 5 10 15  
 Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 206  
 <211> 331  
 <212> DNA  
 <213> Conus striatus

<400> 206  
 cgacctttca agagggatcg atagcagttc gcgatgtcta aactgggggt attgttgacc 60  
 atctgtctgc ttctgtttcc ccttactgct cttccgatgg atgaagatca acctgcagac 120  
 caacttgaag atcgtatgca ggacgacatt tcacttgagc agtatccctc gtttgtagg 180  
 agacaaaagt gttgcggcga aggtcgtca tgccccaaat atttcaaaaa caattttatt 240

tgtggttgtt gttaaataac aacgtgtcga tgaccaactt cggtatcacg actacgcaa 300

gtgtcttgtc taatgataat aaaatgattc c 331

<210> 207

<211> 73

<212> PRT

<213> Conus striatus

<400> 207

Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu  
20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val  
35 40 45

Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe  
50 55 60

Lys Asn Asn Phe Ile Cys Gly Cys Cys  
65 70

<210> 208

<211> 23

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 208

Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn  
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
20

<210> 209

<211> 256

<212> DNA

<213> Conus striatus

<400> 209

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

gacatttcat ctgacgagca tcccttgttt gataagagac aaaactgttg caatggggga 180

tgctccagca aatggtgcag agatcacgca cgttgttgcg gtcgatgata acgtgttgat 240

gaccaacttt ctcgag 256

<210> 210

<211> 75

<212> PRT

<400> 213  
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu  
1 5 10 15  
Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp  
20 25 30  
Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu  
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile  
 50 55 60

Pro Cys Cys Ile  
 65

<210> 214  
 <211> 14  
 <212> PRT  
 <213> Conus tessulatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 214  
 Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile  
 1 5 10

<210> 215  
 <211> 238  
 <212> DNA  
 <213> Conus tessulatus

<400> 215  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtgtgcttct gtttcccctt 60  
 actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacgcagaac 120  
 gagcagcatc ccttgtatga tcagaaaaga aagtgttgcc ggccgccatg cgccatgagc 180  
 tgcggcatgg ctaggtgttg ctattaatga taacgtgttg atgaccaact ttctcgag 238

<210> 216  
 <211> 68  
 <212> PRT  
 <213> Conus tessulatus

<400> 216  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln  
 35 40 45

Lys Arg Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala  
 50 55 60

Arg Cys Cys Tyr  
 65

<210> 217  
 <211> 18  
 <212> PRT  
 <213> Conus tessulatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1

25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 217

Lys Cys Cys Arg Xaa Xaa Cys Ala Met Ser Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Xaa

<210> 218

<211> 564

<212> DNA

<213> Conus textile

<400> 218

gagtcaaccc actgtcacgc caagagcgga cgccacagct aaggcaagaa ggatcgatag 60  
cagttcatga tgtctaaact gggagccttg ttgaccatct gtctacttct gttttccctt 120  
actgctgttc cgctggatgg agatcaacat gcagaccaac ctgcacagcg tctgcaggac 180  
cgcatccaa ctgaagatca tcccttattt gatcccaaca aacggtgttg cccgccggtg 240  
gcatgcaaca tgggatgcaa gccttggttg ggatgaccag ctttgttatc gcggtctcat 300  
gaagtgtcta atgaataagt aaaacgattg cagtttcggt cagatttgct gttgtatttt 360  
ggtctaaaga ttaatgacca aactgttctt ttgatccgga ttttcacgta tttctcgatt 420  
cctattcaac actagataag ttaatcacga cagatctgat tttccatcaa tgccttgctt 480  
tttggctgt catataaatc ttgtttatat ttaatttctc gtcactttca acacgcacac 540  
acacacacac acacacgcgc gcgc 564

<210> 219

<211> 69

<212> PRT

<213> Conus textile

<400> 219

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
20 25 30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe  
35 40 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys  
50 55 60

Lys Pro Cys Cys Gly  
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<210> 220

<211> 16

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

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<210> 221
<211> 780
<212> DNA
<213> Conus textile
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<210> 222
<211> 66
<212> PRT
<213> Conus textile
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<210> 223
<211> 12
<212> PRT
<213> Conus textile
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<220>  
<221> PEPTIDE



<222> (1)..(12)

<223> Xaa at residue 10 is Pro or Hyp

<400> 223

Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys  
1 5 10

<210> 224

<211> 456

<212> DNA

<213> Conus textile

<400> 224

ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt gaagaagggt 60  
ggagagaggt tcatgatgtt gaaaatggga gtggtgctat tcatctttct ggtactgttt 120  
cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc ggagaacaaa 180  
cagctcctca acccagatga aaggagggaa atcctattgc ctgctctgag gaagttctgc 240  
tgtgattcga attggtgcc aatttcggat tgtgagtgt gctacggta gcgccgaaca 300  
tccatggcac tgtgctgggc ggtttcatcc caacaacgac agcgtttggt gatttcatgt 360  
atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420  
ttcgtgttct tttctgacaa taaatgacaa acctcc 456

<210> 225

<211> 70

<212> PRT

<213> Conus textile

<400> 225

Met Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe  
1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr  
20 25 30

Ala Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Leu  
35 40 45

Leu Pro Ala Leu Arg Lys Phe Cys Cys Asp Ser Asn Trp Cys His Asp  
50 55 60

Cys Glu Cys Cys Tyr Gly  
65 70

<210> 226

<211> 17

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 226

Phe Cys Cys Asp Ser Asn Xaa Cys His Ile Ser Asp Cys Xaa Cys Cys  
1 5 10 15

Xaa

<210> 227  
 <211> 456  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> misc\_feature  
 <222> (1)..(456)  
 <223> n may be any nucleotide

<400> 227  
 caaggaacag tcaacccac agccacgcca agagcagaca gccacagcta cgtgaagaag 60  
 ggtggagaga ggttcgtgat gttgaaaatg ggagtgggtgc tattcatctt cctgggtactg 120  
 tttcccctgg caacgctcca gctggatgca gatcaacctg tagaacgata tgcggagaac 180  
 aaacagctcc tcagcccaga tgaaaggagg gaaatcatat tgcattgctct ggggacgcga 240  
 tgctgttctt gggatgtgtg cgaccaccgc agttgtactt gctgcgggta gcgccgaaca 300  
 tccatggcgc tgtgctgggc ggttttatcc caacaacgac agcgtttgtt gatttcatgt 360  
 atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tgggttcagat 420  
 ttcgtgttct tttctgacaa taaatgacaa aacncc 456

<210> 228  
 <211> 70  
 <212> PRT  
 <213> Conus textile

<400> 228  
 Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro  
 1 5 10 15  
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala  
 20 25 30  
 Glu Asn Lys Gln Leu Leu Ser Pro Asp Glu Arg Arg Glu Ile Ile Leu  
 35 40 45  
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro  
 50 55 60  
 Ser Cys Thr Cys Cys Gly  
 65 70

<210> 229  
 <211> 15  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo  
 -Tr

<400> 229  
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys  
 1 5 10 15

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<210> 230  
 <211> 235  
 <212> DNA  
 <213> Conus textile

<400> 230  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctcttc cgctggatgg agatcaaccc gcagaccaag ctgcagagcg tatgcaggcc 120  
 gagcagcatc ccttgtttga tcagaaaaga cgggtgtgca agtttccatg ccccgatagt 180  
 tgcagatatt tgtgttgcg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 231  
 <211> 67  
 <212> PRT  
 <213> Conus textile

<400> 231  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30  
 Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln  
 35 40 45  
 Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu  
 50 55 60  
 Cys Cys Gly  
 65

<210> 232  
 <211> 16  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 232  
 Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys  
 1 5 10 15

<210> 233  
 <211> 321  
 <212> DNA  
 <213> Conus tulipa

<400> 233  
 cgacctcaag agggatcgat agcagttcat gtctaaactg \_yagtcttgt tgacaatctg 60  
 tctgcttctg tttcccctta ctgctctgcc gatggatgga gatgaacctg cagaccgacc 120  
 tgcagagcgt atgcaggaca acatttcatc tgagcagcat cccttgtttg aggagagaca 180  
 cggatgttgc aaggggcccg aaggatgctc ctccagagaa tgcagacccc aacattgttg 240



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<400>      240
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu Leu Phe
 1              5              10              15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Ala Asp Gln Pro
      20              25              30

Ala Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Met Asn Pro Trp Phe
 35              40              45

Asp Pro Val Lys Arg Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro
 50              55              60

Cys Cys Pro

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65

<210> 241  
 <211> 14  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 241  
 Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa  
 1 5 10

<210> 242  
 <211> 286  
 <212> DNA  
 <213> Conus figulinus

<400> 242  
 caagagggat cgatagcagt tcatgatgtc taaactgaga gtcttggtga ccttatgtct 60  
 gcttctgttt ccccttactg ctcttccgct gaatgaagat caacctgcag agcgtatgca 120  
 ggacgacaat tcatctgagc agcaccocctt gtatgaccac aaacgaaagt gttgccggtg 180  
 gccatgcccc gcaagatgcg gctcttggtg cctgtaataa cgtgttggcc aactttgtta 240  
 tcacggccac gtcaaagtgt taatgaataa gtaaaacgat tgcagt 286

<210> 243  
 <211> 64  
 <212> PRT  
 <213> Conus figulinus

<400> 243  
 Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met  
 20 25 30

Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg  
 35 40 45

Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu  
 50 55 60

<210> 244  
 <211> 15  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 5 and 7 is Pro c. Hyp; Xaa at residue 4 is Trp or bromo-Tr

<400> 244  
 Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu  
 1 5 10 15

<210> 245

<211> 301  
 <212> DNA  
 <213> Conus figulinus

<400> 245  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgttga ccttatgtct 60  
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caagctgcag accgacctgc 120  
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacgggtg 180  
 ttgcgagttg tcaagctgcc ttggatgcgt cccttgttgc acatcttaat aacgtgtgga 240  
 tgaccaactg tgttatcacg gccacgtcaa gtgtctaata aataagtaaa atgattgcag 300  
 t 301

<210> 246  
 <211> 68  
 <212> PRT  
 <213> Conus figulinus

<400> 246  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp  
 35 40 45  
 Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro  
 50 55 60  
 Cys Cys Thr Ser  
 65

<210> 247  
 <211> 16  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 3 and 12 is Pro or Hyp

<400> 247  
 Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser  
 1 5 10 15

<210> 248  
 <211> 301  
 <212> DNA  
 <213> Conus figulinus

<400> 248  
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccttatgtct 60  
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120  
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacgggtg 180  
 ttgcgagttg tcaaaatgcc atggatgcgt cccttgttgc ataccttaat aacgtgcgga 240

tgaccaactg tgttatcacg gccacgtcaa gtgtctaatag aataagtaaa atgattgcag 300  
t 301

<210> 249  
<211> 68  
<212> PRT  
<213> Conus figulinus

<400> 249  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp  
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro  
50 55 60  
Cys Cys Ile Pro  
65

<210> 250  
<211> 16  
<212> PRT  
<213> Conus figulinus

<220>  
<221> PEPTIDE  
<222> (1)..(16)  
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 250  
Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa  
1 5 10 15

<210> 251  
<211> 298  
<212> DNA  
<213> Conus quercinus

<400> 251  
caagagggat cgatagcagt tcatgatgtc taaactcgga gtcttgttga ccatctgtct 60  
ggttctgttt ccccttacag ctcttcagct ggatggagat caacctgcag accgacctgc 120  
agagcgtacg caggacattt catctgaaca gtatcgaaaag tttgatcaga gacagaggtg 180  
ttgccggtgg ccatgccccg gtagttgcag atgctgccgt tatcgttaac gtgttggtga 240  
ccagctttgt tatcacgacc acgccaagtg tctaacgaat aagtaaaatg attgcagt 298

<210> 252  
<211> 68  
<212> PRT  
<213> Conus quercinus

<400> 252  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro



30

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser  
50 55 60

<220>

Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg  
50 55 60



<211> 23  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 266  
 Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
 20

<210> 267  
 <211> 239  
 <212> DNA  
 <213> Conus betulinus

<400> 267  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctgttc cgttggatgg agatcaacct gcagaccaac ctgcagagcg tatgcagaac 120  
 gagcagcatc cctcgtttga tcagaaaaga aggtgctgcc ggtggccatg cccaggtata 180  
 tgcggcatgg ctaggtgttg cttcgtcatg ataacgtgtt gatgaccaac tttctcgag 239

<210> 268  
 <211> 71  
 <212> PRT  
 <213> Conus betulinus

<400> 268  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg  
 35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
 50 55 60

Cys Phe Val Met Ile Thr Cys  
 65 70

<210> 269  
 <211> 23  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or  
 bromo-Tr

<400> 269  
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys  
 1 5 10 15



<400> 273  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120  
 aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggaggctg ttgcacacct 180  
 ccgaagaaat gcaaagaccg agcctgcaaa cctgcacggt gctgcggccc aggataacgt 240  
 gttgatgacc aactttctcg cc 262

<210> 274  
 <211> 76  
 <212> PRT  
 <213> Conus parius

<400> 274  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30  
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp  
 50 55 60  
 Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
 65 70 75

<210> 275  
 <211> 24  
 <212> PRT  
 <213> Conus parius

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 275  
 Arg Gly Gly Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Ala Cys  
 1 5 10 15  
 Lys Xaa Ala Arg Cys Cys Gly Xaa  
 20

<210> 276  
 <211> 259  
 <212> DNA  
 <213> Conus parius

<400> 276  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatgcaggac 120  
 aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cacacctcgg 180  
 aggaaatgca aagaccgagc ctgcaaacct gcacgttggt gcggcccagg ataacgtggt 240  
 gatgaccaac tttctcgag 259

<210> 277  
 <211> 75  
 <212> PRT  
 <213> Conus parius

<400> 277  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30  
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg  
 50 55 60  
 Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
 65 70 75

<210> 278  
 <211> 23  
 <212> PRT  
 <213> Conus parius

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 278  
 Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys  
 1 5 10 15  
 Xaa Ala Arg Cys Cys Gly Xaa  
 20

<210> 279  
 <211> 241  
 <212> DNA  
 <213> Conus coronatus

<400> 279  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60  
 actgcccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgctgcga ttggccatgc 180  
 atcccaggat gcaccccttg ttgcttgcct tgataacgtg ttgatgacca actttctcga 240  
 g 241

<210> 280  
 <211> 68  
 <212> PRT  
 <213> Conus coronatus

<400> 280  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
 20 25 30



<210>	284
<211>	14
<212>	PRT

<220>

<222> (1) . . (14)

<400> 284

<210> 285

<212> PRT

 $\langle 220 \rangle$ 

<222> (1) .. (14)

<400> 285

<210> 286

<212> PRT

 $\langle 220 \rangle$ 

<222> (1) . . (14)

<400> 286

<210> 287

$\langle 211 \rangle$  235

<212> DNA

<400> 287

actgctcttc cgctggatgg agatcaacct gcataccaag ctgcagagcg tatgcaggcc 120

gagcatcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180

tgcaaatatt tgtgttgctg gtgatgataa catgttgatg accaactttc ttgaq 235

<210> 288

<211> 65

<212> PRT

<213> Conus pennaceus

<400> 288

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Cys Cys Phe  
65

<210> 292  
 <211> 14  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 292  
 Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
 1 5 10

<210> 293  
 <211> 244  
 <212> DNA  
 <213> Conus pulicarius

<400> 293  
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtgtccctt 60  
 actgctcttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat 120  
 gacacttcag ctgcacagat tttcgggttt gatcccgctca aacggtgctg caaattgcta 180  
 tgctactcgg gatgcactcc ttgttgccat atttgataac gtgttgatga ccaactttct 240  
 cgag 244

<210> 294  
 <211> 67  
 <212> PRT  
 <213> Conus pulicarius

<400> 294  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Cys  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe  
 35 40 45  
 Asp Pro Val Lys Arg Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys  
 50 55 60  
 Cys His Ile  
 65

<210> 295  
 <211> 16  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 295  
 Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile

1 5 10 15

<210> 296  
 <211> 259  
 <212> DNA  
 <213> Conus rattus

<400> 296  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttgt gtttccgctt 60  
 actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgtagagcg tatacaggac 120  
 aacatttcac ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cgcacctccg 180  
 aggaaatgca aagaccgagc ctgcaaacct gcacgttgct gcggcccagg ataacgtggt 240  
 gatgaccaac tttctcgag 259

<210> 297  
 <211> 75  
 <212> PRT  
 <213> Conus rattus

<400> 297  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Val Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30  
 Val Glu Arg Ile Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Glu Lys Arg Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg  
 50 55 60  
 Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
 65 70 75

<210> 298  
 <211> 23  
 <212> PRT  
 <213> Conus rattus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 298  
 Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys  
 1 5 10 15  
 Xaa Ala Arg Cys Cys Gly Xaa  
 20

<210> 299  
 <211> 262  
 <212> DNA  
 <213> Conus stercusmuscarum

<400> 299  
 ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt 60  
 attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

gacatttcat ctgagaagca tcccttggtt gataagagac aacggtgttg caatgggchg 180  
 aggggatgct ccagcagatg gtgcagagat cactcacgtt gttgcggtcg acgataacgt 240  
 gttgatgacc aactttctcg ag 262

<210> 300  
 <211> 76  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 300  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Ile Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Lys His Pro Leu Phe  
 35 40 45  
 Asp Lys Arg Gln Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg  
 50 55 60  
 Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 301  
 <211> 22  
 <212> PRT  
 <213> Conus stercusmuscarum  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Trp or  
 bromo-Tr

<400> 301  
 Xaa Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Xaa Cys Arg  
 1 5 10 15  
 Asp His Ser Arg Cys Cys  
 20

<210> 302  
 <211> 241  
 <212> DNA  
 <213> Conus ebraceus

<400> 302  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgtttct gtttccctt 60  
 actgtctctt cactggatga aggtcaacct gcagacctac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgttgcca gcagccatgc 180  
 tacatgggat gcatcccttg ttgtttctaa taataacgtg ttgatgacca actttctcga 240  
 g 241

<210> 303  
 <211> 67  
 <212> PRT



50

55

60

Cys Cys Phe  
65

<210> 307  
<211> 15  
<212> PRT  
<213> Conus ebraceus

<220>  
<221> PEPTIDE  
<222> (1)..(15)  
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1  
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 307  
Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
1 5 10 15

<210> 308  
<211> 238  
<212> DNA  
<213> Conus flavidus

<400> 308  
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
actgctgttc cgttggatgg agatcaacct gcagaccagc ctgcagagcg tatgcagaac 120  
gagcagcatc ccttgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata 180  
tgcggcatgg ctaggtgttg ctggtcatga taacgtgttg atgaccaact ttctcgag 238

<210> 309  
<211> 67  
<212> PRT  
<213> Conus flavidus

<400> 309  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro  
20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Leu Phe Asp Gln Lys Arg  
35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
50 55 60

Cys Ser Ser  
65

<210> 310  
<211> 19  
<212> PRT  
<213> Conus flavidus

<220>  
<221> PEPTIDE  
<222> (1)..(19)  
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or



bromo-Tr

&lt;400&gt; 310

Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys  
 1 5 10 15

Cys Ser Ser

&lt;210&gt; 311

&lt;211&gt; 245

&lt;212&gt; DNA

&lt;213&gt; Conus miliaris

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(245)

&lt;223&gt; n may be any nucleotide

&lt;400&gt; 311

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60  
 actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcca ttggccatgc 180  
 agcgcaggat gctacccttg ttgcttcctt taataacgtg ttgatgacca actnangnaa 240  
 aaaaaa 245

&lt;210&gt; 312

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Conus miliaris

&lt;400&gt; 312

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro  
 50 55 60

Cys Cys Phe Pro  
 65

&lt;210&gt; 313

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus miliaris

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

<223> Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Tr  
 p or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr  
 , di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 313

Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa  
 1 5 10 15

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<220>
<221> misc_feature
<222> (1)..(230)
<223> n may be any nucleotide
<400> 314
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```
<210> 315
<211> 66
<212> PRT
<213> Conus miliaris
```

```
<210> 316
<211> 16
<212> PRT
<213> Conus miliaris
```

<400> 316  
Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arg  
1 5 10 15

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<400> 317
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct    60
gcttctgttt ccccttactg ctcttcgcgt ggatggagat caacctgcag accaagctgc    120
```

agagcgtatg caggccgagc agcatccctt gtttgatcag aaaagacggt gttgcaggtt 180

tccatgcccc gatacttgca gacatttggtg ttgcgggtga tgataacgtg ctgatgaccc 240

actttgtcat cacggctacg tcaagtgtct aatgaataa; taaaatgatt gcagt 295

<210> 318

<211> 65

<212> PRT

<213> Conus ammiralis

<400> 318

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala  
20 25 30

Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg  
35 40 45

Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys  
50 55 60

Gly  
65

<210> 319

<211> 16

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 and 8 is Pro or Hyp

<400> 319

Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys  
1 5 10 15

<210> 320

<211> 267

<212> DNA

<213> Conus ammiralis

<400> 320

caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgctga ccatctgtct 60

acttctgttt tcccttaatg ctgttccgct ggatggagat caacctgcag accaacctgc 120

agagcgtctg ctggacgaca tttcatctga aaataatccc ttttatgatc ccgccaaacg 180

gtgttgcatg acttgcttcg gttgcacacc ttgttggtga tgaccagcct catcaagtgt 240

ctaacgaata agtaaaacga ttgcagt 267

<210> 321

<211> 66

<212> PRT

<213> Conus ammiralis

<400> 321

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

$\langle 210 \rangle$	325
$\langle 211 \rangle$	18

<212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 325  
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile  
 1 5 10 15

Phe Ser

<210> 326  
 <211> 284  
 <212> DNA  
 <213> Conus ammiralis

<400> 326  
 caagagggat cgatagcagt tcatgatgtt taaactcgga gtcttgctga ccatctgtct 60  
 acttctgttt tocctaattg ctgttccgct ggatggagat caacatgcag accaacctgc 120  
 agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgata ccgtcaaacg 180  
 gtgttgacagg ttgttatgcc tcagttgcaa cccttggtgt ggatgaccag ctttgttatc 240  
 acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284

<210> 327  
 <211> 67  
 <212> PRT  
 <213> Conus ammiralis

<400> 327  
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45  
 Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro  
 50 55 60

Cys Cys Gly  
 65

<210> 328  
 <211> 13  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 11 is Pro or Hyp

<400> 328

<210> 329  
<211> 289  
<212> DNA  
<213> *Conus ammiralis*

<400>	329						
caagaaggat	cgatagcagt	tcatgatgtc	taaactggga	gccttgttga	ccatctgtct		60
acttctgttt	tcccttactg	ctgttcgcgt	ggatggagat	caacatgcag	accaacctgc		120
agagcgtctg	caggaccgca	ttccaactga	agatcatccc	ttatttgatc	ccaacaaacg		180
gtgttgcgat	gattcggaat	gcggctattc	atgctggcct	tgctgttatg	gataagcttt		240
gttatcgcg	cctcatccag	tgtcaacgaa	taagtaaac	gattgcagt			289

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<210> 330
<211> 70
<212> PRT
<213> Conus ammiralis
```

```

<400>      330
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1          5          10          15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
      20          25          30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
      35          40          45

Asp Pro Asn Lys Arg Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys
      50          55          60

Trp Pro Cys Cys Tyr Gly
65          70

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```
<210> 331
<211> 16
<212> PRT
<213> Conus ammiralis
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<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13 i
s Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at resid
ue 9 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulph
o-Tyr or O-phospho-Ty
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<400> 331  
Cys Cys Asp Asp Ser Xaa Cys Gly Xaa Ser Cys Xaa Xaa Cys Cys Xaa  
1 5 10 15

<210>	332
<211>	272
<212>	DNA
<213>	Conus spurius

<400> 332  
Caagaaggat cgatagcagt tcattgatgtc taaactggga gtcttgctga ccattctgtct 60

gcttctgttt ccacgtactt ctcttccgct ggatggagat caacctgcag tccgatctgc 120  
 aaagcgtatg cattcatcta tacagcgtcg tttctttgat cccgtcaaac ggtgttgccc 180  
 tagatgcagc gagtgaacc cttgttgtgg atgaccagct ttgtcatcgc ggcctcatta 240  
 agtgtctaata gaataagtaa aatgattgca gt 272

<210> 333  
 <211> 63  
 <212> PRT  
 <213> Conus spurius

<400> 333  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Arg Thr Ser Leu Pro Leu Asp Gly Asp Gln Pro Ala Val Arg Ser  
 20 25 30  
 Ala Lys Arg Met His Ser Ser Ile Gln Arg Arg Phe Phe Asp Pro Val  
 35 40 45  
 Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly  
 50 55 60

<210> 334  
 <211> 12  
 <212> PRT  
 <213> Conus spurius  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 10 is Pro or Hy

<400> 334  
 Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys  
 1 5 10

<210> 335  
 <211> 293  
 <212> DNA  
 <213> Conus omaria

<400> 335  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtctcgttga ccatctgtct 60  
 acttctattt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaata ccgtaaacg 180  
 gtgttgcatg gaggaagaat gcagcagtgc atgctggcct tgttgttggg ggtgatcagc 240  
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aatgattgc agt 293

<210> 336  
 <211> 70  
 <212> PRT  
 <213> Conus omaria

<400> 336  
 Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Cys Thr Pro Cys Asp Cys  
65 70



<210> 340  
 <211> 17  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo-  
 -Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Ty

<400> 340  
 Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp  
 1 5 10 15

Cys

<210> 341  
 <211> 290  
 <212> DNA  
 <213> Conus omaria

<400> 341  
 caagagggat cgatagcagt tcatgatgtc tatactggga gtcttggtga tcatctgtct 60  
 acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120  
 agagcgtatg caggacggca tttcatctga acatcatccc tttttggatc ccgtaaacg 180  
 gtgttgccat ctattggcat gccgctttgg atgctgcct tgttggtggt gaccagcttt 240  
 gttatcgcg g cctcatcaag tgtctaataa ataagtaaaa cgattgcagt 290

<210> 342  
 <211> 69  
 <212> PRT  
 <213> Conus omaria

<400> 342  
 Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys  
 1 5 10 15  
 Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu  
 35 40 45  
 Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys  
 50 55 60

Ser Pro Cys Cys Trp  
 65

<210> 343  
 <211> 16  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or bromo-  
 o-Tr

Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa  
1 5 10 15

<213> Conus omaria

tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<213> Conus omaria

Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys  
1 5 10 15

Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe  
35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly  
50 55 60

Cys Thr Pro Cys Gly Cys  
65 70

<213> Conus omaria

<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly  
1 5 10 15

Cys

<213> Conus episcopatus

<400> 347  
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180  
 gtgttgcgat gaggacgaat gcaacagttc atgctggcct tgttggtggg ggtgatcagc 240  
 tttgttatcg cggcctgac aagtgtataa tgaataagta aaacgattgc agt 293

<210> 348  
 <211> 70  
 <212> PRT  
 <213> Conus episcopatus

<400> 348  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45  
 Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys  
 50 55 60  
 Trp Pro Cys Cys Trp Gly  
 65 70

<210> 349  
 <211> 16  
 <212> PRT  
 <213> Conus episcopatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 349  
 Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa  
 1 5 10 15

<210> 350  
 <211> 293  
 <212> DNA  
 <213> Conus episcopatus

<400> 350  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180  
 gtgttgcgat gaggacgaat gcagcagttc atgctggcct tgttggtggg gatgagcagc 240  
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 351  
 <211> 70

<212> PRT  
 <213> Conus episcopatus

<400> 351  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45  
 Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys  
 50 55 60  
 Trp Pro Cys Cys Trp Gly  
 65 70

<210> 352  
 <211> 16  
 <212> PRT  
 <213> Conus episcopatus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 352  
 Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa  
 1 5 10 15

<210> 353  
 <211> 290  
 <212> DNA  
 <213> Conus episcopatus

<400> 353  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccattctgtct 60  
 atttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180  
 gtgttgcccc gggcgcat gtgccatggg atgcaagcct tgttggtgat gagcagcttt 240  
 gttatcgtgg cctcatcaag tgtctaata gaataagtaaaa cgattgcagt 290

<210> 354  
 <211> 69  
 <212> PRT  
 <213> Conus episcopatus

<400> 354  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45

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<220>
<221>  PEPTIDE
<222>  (1)..(16)
<223>  Xaa at residue 5 and 6 is Pro or Hyp
```

<400> 358  
 Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys  
 1 5 10 15

<210> 359  
 <211> 290  
 <212> DNA  
 <213> Conus aulicus

<400> 359  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
 acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180  
 gtgttgccga cgggtggcat gtgccatggg atgcaagcct tgttggtgat gacgagcttt 240  
 gttatcgtgg cctcatcaag tgtctaataa ataagtaaaa tgattgcagt 290

<210> 360  
 <211> 69  
 <212> PRT  
 <213> Conus aulicus

<400> 360  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45  
 Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys  
 50 55 60  
 Lys Pro Cys Cys Gly  
 65

<210> 361  
 <211> 15  
 <212> PRT  
 <213> Conus aulicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 361  
 Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys  
 1 5 10 15

<210> 362  
 <211> 290  
 <212> DNA  
 <213> Conus aulicus

<400> 362  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga tcatctgtct 60  
 acttctgtct ccccttactg ctgttccgct ggatggagat caacctgcag accgacctgc 120

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<210> 363
<211> 69
<212> PRT
<213> Conus aulicus
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<210> 364
<211> 16
<212> PRT
<213> Conus aulicus
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<220>
<221>  PEPTIDE
<222>  (1)..(16)
<223>  Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 13 is Glu or
gamma-carboxy Glu; Xaa at residue 4 and 14 is Pro or Hy

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<400> 364  
Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys  
1 5 10 15

<210>	365
<211>	293
<212>	DNA
<213>	Conus aureus

<400>	365						
caagaaggat	cgatagcagt	tcattgatgtc	taaactggga	gccttggtga	ccatctgtct		60
acttctgttt	tcccttactg	ctgttccgct	ggatggagat	caacatgcag	accaacatgc		120
agagcgtctg	catgaccgcc	ttccaactga	aaatcatccc	ttatatgata	ccgtcaaacg		180
gtgttgcgat	gattcggaat	gcgactattc	ttgctggcct	tgctgtattt	ttggataacc		240
tttgttatcg	cggcctcatc	aagtgtcaaa	tgaataagta	aaacgattgc	agt		293

<210>	366
<211>	71
<212>	PRT
<213>	Conus aureus

<400> 366

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln His  
 20 25 30  
 Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45  
 Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys  
 50 55 60  
 Trp Pro Cys Cys Ile Phe Gly  
 65 70

<210> 367  
 <211> 17  
 <212> PRT  
 <213> Conus aureus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 367  
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile  
 1 5 10 15

Phe

<210> 368  
 <211> 290  
 <212> DNA  
 <213> Conus aureus

<400> 368  
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccattctgtct 60  
 acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120  
 agagcgtctg caggaccgca ttccaactga aaatcatccc ttatttgatc cgaacaaacg 180  
 gtgttgcaat gattgggaat gcgacgattc atgctggcct tgctgttatg gataaccttt 240  
 gttatcgcgg cctcatcaag tgtcaaatga ataagtaaaa cgattgcagt 290

<210> 369  
 <211> 70  
 <212> PRT  
 <213> Conus aureus

<400> 369  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe  
 35 40 45





<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 373

Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser  
1 5 10 15

Gln Ile Cys His Cys Cys  
20

<210> 374

<211> 315

<212> DNA

<213> Conus consors

<400> 374

taagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60  
gcttctgttt ccccttattg ctcttccaat ggatggagat caacctgcag accgacctgc 120  
agagcgtatg caggacgaca tttcatctca gcagcatccc ttgtttgata agagaggccg 180  
ctgttgcgat gtgccgaacg catgctccgg cagatggtgc agagatcacg cacaatgttg 240  
cggatgacga taacgtgttg atgaccaact ttgtgatcac ggctacatca agtgaataag 300  
taaaacgatt gcagt 315

<210> 375

<211> 74

<212> PRT

<213> Conus consors

<400> 375

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe  
35 40 45

Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg  
50 55 60

Trp Cys Arg Asp His Ala Gln Cys Cys Gly  
65 70

<210> 376

<211> 22

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

&lt;400&gt; 376

Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg  
 1 5 10 15

Asp His Ala Gln Cys Cys  
 20

&lt;210&gt; 377

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Conus consors

&lt;400&gt; 377

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ctgtctgttt 60  
 gcttctgttt ccccttactg ctcttccgat ggatggagat caacctgcag accaacctgc 120  
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttgata agagacaaag 180  
 gtgttgcaact gggaagaagg ggtcatgctc cggtaaagca tgcaaaagtc tcaaagtgtg 240  
 ctctggacga taactgtgtg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300  
 gaataagtaa aacgattgca gt 322

&lt;210&gt; 378

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;400&gt; 378

Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe  
 35 40 45

Asp Lys Arg Gln Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly  
 50 55 60

Lys Ala Cys Lys Ser Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

&lt;210&gt; 379

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

&lt;223&gt; Xaa at residue 1 is Gln or pyro-Glu

&lt;400&gt; 379

Xaa Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Ser Leu Lys Cys Cys Ser  
 20

&lt;210&gt; 380



$\langle 210 \rangle$	391
$\langle 211 \rangle$	14

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<210> 397
<211> 16
<212> PRT
<213> Conus textile
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Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys Gly  
1 5 10 15

<213> Conus marmoreus

<223> Xaa is Hyp

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa  
1 5 10 15

<213> Conus capitaneus

Ser Cys Cys Arg Asp Cys Gly Glu Asp Cys Val Gly Cys Cys Arg  
1 5 10 15

<213> Conus coronatus

Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro Cys Cys Leu Pro  
1 5 10 15

<213> Conus dalli

Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile  
1 5 10 15

<213> Conus dalli

Glx Gln Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Glu Pro Cys  
1 5 10 15

<213> Conus dalli

&lt;400&gt; 403

Cys	Cys	Asn	Ala	Gly	Phe	Cys	Arg	Phe	Gly	Cys	Thr	Pro	Cys	Cys	Trp
1				5					10					15	

&lt;210&gt; 404

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus distans

&lt;400&gt; 404

Glx	Cys	Cys	Val	His	Pro	Cys	Pro	Cys	Thr	Pro	Cys	Cys	Arg
1				5					10				

&lt;210&gt; 405

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus figulinus

&lt;400&gt; 405

Cys	Cys	Pro	Trp	Pro	Cys	Asn	Ile	Gly	Cys	Val	Pro	Cys	Cys
1				5					10				

&lt;210&gt; 406

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus figulinus

&lt;400&gt; 406

Cys	Cys	Ser	Lys	Asn	Cys	Ala	Val	Cys	Ile	Pro	Cys	Cys	Pro
1				5					10				

&lt;210&gt; 407

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Conus figulinus

&lt;400&gt; 407

Cys	Cys	Arg	Trp	Pro	Cys	Pro	Ala	Arg	Cys	Gly	Ser	Cys	Cys	Leu
1				5					10					15

&lt;210&gt; 408

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus figulinus

&lt;400&gt; 408

Cys	Cys	Glu	Leu	Ser	Arg	Cys	Leu	Gly	Cys	Val	Pro	Cys	Cys	Thr	Ser
1				5					10					15	

&lt;210&gt; 409

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus figulinus

&lt;400&gt; 409

Cys	Cys	Glu	Leu	Ser	Lys	Cys	His	Gly	Cys	Val	Pro	Cys	Cys	Ile	Pro
1				5					10					15	

&lt;210&gt; 410

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus generalis

&lt;400&gt; 410



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<210> 417
<211> 19
<212> PRT
<213> Conus leopardus
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Cys Cys His

Cys Cys His

Val

Cys Cys Trp

Cys

<400> 423

<400> 429

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn  
1 5 10 15

<210> 430  
<211> 15  
<212> PRT  
<213> Conus quercinus

<220>  
<221> PEPTIDE  
<222> (1)..(15)  
<223> Xaa is Hyp

<400> 430  
Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn  
1 5 10 15

<210> 431  
<211> 16  
<212> PRT  
<213> Conus rattus

<400> 431  
Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln  
1 5 10 15

<210> 432  
<211> 20  
<212> PRT  
<213> Conus striatus

<400> 432  
Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His  
1 5 10 15

Ala Arg Cys Cys  
20

<210> 433  
<211> 12  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(12)  
<223> Xaa is Hyp

<400> 433  
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys  
1 5 10

<210> 434  
<211> 14  
<212> PRT  
<213> Conus tessulatus

<400> 434  
Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile  
1 5 10

<210> 435  
<211> 18  
<212> PRT  
<213> Conus tessulatus

&lt;400&gt; 435

Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala Arg Cys  
 1 5 10 15

Cys Tyr

&lt;210&gt; 436

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus betulinus

&lt;400&gt; 436

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
 1 5 10 15

Cys Phe Val Met Ile Thr Cys  
 20

&lt;210&gt; 437

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus betulinus

&lt;400&gt; 437

Arg Cys Cys Arg Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys  
 1 5 10 15

Cys Phe Val Met Ile Thr Cys  
 20

&lt;210&gt; 438

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 438

Phe Cys Cys Asp Ser Asn Trp Cys His Asp Cys Glu Cys Cys Tyr  
 1 5 10 15

&lt;210&gt; 439

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 439

Cys Cys His Trp Asn Trp Cys Asp His Leu Cys Ser Cys Cys Gly Ser  
 1 5 10 15

&lt;210&gt; 440

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 440

Asp Cys Cys Xaa Leu Pro Ala Cys Pro Phe Gly Cys Asn Xaa Cys Cys  
 1 5 10 15

&lt;210&gt; 441

&lt;211&gt; 16

<212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa is Hyp

<400> 441  
 Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg  
 1 5 10 15

<210> 442  
 <211> 16  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa is Hyp

<400> 442  
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg  
 1 5 10 15

<210> 443  
 <211> 16  
 <212> PRT  
 <213> Conus marmoreus

<400> 443  
 Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Arg  
 1 5 10 15

<210> 444  
 <211> 17  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa is Hyp

<400> 444  
 Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys  
 1 5 10 15

Val

<210> 445  
 <211> 15  
 <212> PRT  
 <213> Conus textile

<400> 445  
 Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys  
 1 5 10 15

<210> 446  
 <211> 16  
 <212> PRT  
 <213> Conus textile

&lt;400&gt; 446

Arg	Cys	Cys	Lys	Phe	Pro	Cys	Pro	Asp	Ser	Cys	Arg	Tyr	Leu	Cys	Cys
1				5					10					15	

&lt;210&gt; 447

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus aureus

&lt;400&gt; 447

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Phe

&lt;210&gt; 448

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus aureus

&lt;400&gt; 448

Cys	Cys	Asn	Asp	Trp	Glu	Cys	Asp	Asp	Ser	Cys	Trp	Pro	Cys	Cys	Tyr
1				5					10					15	

&lt;210&gt; 449

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 449

Arg	Cys	Cys	Arg	Phe	Pro	Cys	Pro	Asp	Thr	Cys	Arg	His	Leu	Cys	Cys
1				5					10					15	

&lt;210&gt; 450

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 450

Cys	Cys	Met	Thr	Cys	Phe	Gly	Cys	Thr	Pro	Cys	Cys
1				5					10		

&lt;210&gt; 451

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 451

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Phe Ser

&lt;210&gt; 452

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 452

Cys	Cys	Arg	Leu	Leu	Cys	Leu	Ser	Cys	Asn	Pro	Cys	Cys
1				5					10			

&lt;210&gt; 453

&lt;211&gt; 16

&lt;212&gt; PRT

<213> Conus ammiralis

<400> 453

Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys Trp Pro Cys Cys Tyr  
1 5 10 15

<210> 454

<211> 16

<212> PRT

<213> Conus aulicus

<400> 454

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys  
1 5 10 15

<210> 455

<211> 15

<212> PRT

<213> Conus aulicus

<400> 455

Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys Lys Pro Cys Cys  
1 5 10 15

<210> 456

<211> 16

<212> PRT

<213> Conus aulicus

<400> 456

Glx Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys Glu Pro Cys Cys  
1 5 10 15

<210> 457

<211> 18

<212> PRT

<213> Conus emaciatus

<400> 457

Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys Cys Pro Tyr Gly  
1 5 10 15

Ser Pro

<210> 458

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 458

Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp  
1 5 10 15

<210> 459

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 459

Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys Trp Pro Cys Cys Trp  
1 5 10 15

<210> 460

<211> 15

<212> PRT



<213> Conus episcopatus

<400> 460

Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys Lys Pro Cys Cys  
1 5 10 15

<210> 461

<211> 16

<212> PRT

<213> Conus omaria

<400> 461

Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp  
1 5 10 15

<210> 462

<211> 16

<212> PRT

<213> Conus omaria

<400> 462

Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys Trp  
1 5 10 15

<210> 463

<211> 12

<212> PRT

<213> Conus spurius

<400> 463

Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys  
1 5 10

<210> 464

<211> 16

<212> PRT

<213> Conus pennaceus

<400> 464

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys  
1 5 10 15

<210> 465

<211> 19

<212> PRT

<213> Conus flavidus

<400> 465

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Ser Ser

<210> 466

<211> 14

<212> PRT

<213> Conus pulicarius

<400> 466

Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys Cys His Ile  
1 5 10

<210> 467

<211> 15

<212> PRT

<213> Conus ebraceus

<400> 467

Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
1 5 10 15

<210> 468

<211> 15

<212> PRT

<213> Conus ebraceus

<400> 468

Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
1 5 10 15

<210> 469

<211> 14

<212> PRT

<213> Conus pulicarius

<400> 469

Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
1 5 10

<210> 470

<211> 16

<212> PRT

<213> Conus miliaris

<400> 470

Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro Cys Cys Phe Pro  
1 5 10 15

<210> 471

<211> 16

<212> PRT

<213> Conus miliaris

<400> 471

Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys Phe Arg  
1 5 10 15

<210> 472

<211> 23

<212> PRT

<213> Conus rattus

<400> 472

Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys  
1 5 10 15

Pro Ala Arg Cys Cys Gly Pro  
20

<210> 473

<211> 22

<212> PRT

<213> Conus stercusmuscarum

<400> 473

Glx Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Trp Cys Arg  
1 5 10 15

Asp His Ser Arg Cys Cys  
20

<210> 474  
 <211> 22  
 <212> PRT  
 <213> Conus consors

<400> 474  
 Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg  
 1 5 10 15  
 Asp His Ala Gln Cys Cys  
 20

<210> 475  
 <211> 23  
 <212> PRT  
 <213> Conus consors

<400> 475  
 Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15  
 Lys Ser Leu Lys Cys Cys Ser  
 20

<210> 476  
 <211> 22  
 <212> PRT  
 <213> Conus aurisiacus

<400> 476  
 Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser  
 1 5 10 15  
 Gln Ile Cys His Cys Cys  
 20

<210> 477  
 <211> 19  
 <212> PRT  
 <213> Conus aurisiacus

<400> 477  
 Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly  
 1 5 10 15  
 Cys Cys Leu

<210> 478  
 <211> 22  
 <212> PRT  
 <213> Conus bullatus

<400> 478  
 Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser  
 1 5 10 15  
 Gln Ile Cys Ala Cys Cys  
 20

<210> 479  
 <211> 21  
 <212> PRT  
 <213> Conus characteristicus

<400> 479

123 474 475 476 477 478 479

Asn Phe Ile Cys Gly Cys  
20



&lt;400&gt; 490

Glx	Lys	Cys	Cys	Thr	Gly	Lys	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

&lt;210&gt; 491

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 491

Glx	Lys	Cys	Cys	Thr	Gly	Arg	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

&lt;210&gt; 492

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;400&gt; 492

Val	Thr	Asp	Arg	Cys	Cys	Lys	Gly	Lys	Arg	Glu	Cys	Gly	Arg	Trp	Cys
1				5					10					15	

Arg	Asp	His	Ser	Arg	Cys	Cys
			20			

&lt;210&gt; 493

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;400&gt; 493

Val	Gly	Asp	Arg	Cys	Cys	Lys	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Trp	Cys
1				5					10					15	

Arg	Asp	His	Ser	Arg	Cys	Cys
			20			

&lt;210&gt; 494

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;400&gt; 494

Val	Gly	Glu	Arg	Cys	Cys	Lys	Asn	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Trp
1				5					10					15	

Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
			20				

&lt;210&gt; 495

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;400&gt; 495

Ile	Val	Asp	Arg	Cys	Cys	Asn	Lys	Gly	Asn	Gly	Lys	Arg	Gly	Cys	Ser
1				5					10					15	

Arg	Trp	Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

25

```

<400> 496
Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp Arg
1      5      10      15
Trp Cys Glu Lys Asn Ser Arg Cys Cys
      20      25

```

```

<400> 497
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15
Pro Gln Arg Cys Cys Ala
20

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<400> 498.  
Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp Arg Ala Cys  
1 5 10 15  
Lys Pro Gln Arg Cys Cys Gly  
20

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<400> 499
Glx Arg Leu Cys Cys Gly Phe Pro Lys Ser Cys Arg Ser Arg Gln Cys
1          5          10          15
Lys Pro His Arg Cys Cys
          20

```

```

<400> 500
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
1          5          10          15
Pro Ala Arg Cys Cys Gly
          20

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<210>	501
<211>	22
<212>	PRT

<400> 501

Met Arg Lys Ala Cys Cys  
20

<210> 502

<211> 22

<212> PRT

<213> Conus laterculatus

<400> 502

Lys Arg Lys Ala Cys Cys  
20

<210> 503

<211> 22

<212> PRT

<213> Conus geographus

 $\langle 220 \rangle$ 

&lt;221&gt; PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (22)$ 

<223> Xaa is Hyp

<400> 503

Xaa Gln Arg Cys Cys Ala  
20

<210> 504

<211> 22

<212> PRT

<213> Conus geographus

 $\langle 220 \rangle$ 

<221> PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (22)$ 

<223> Xaa is Hyp

<400> 504

Xaa Met Lys Cys Cys Ala  
20

<210> 505

<211> 22

<212> PRT

<213> Conus geographus

 $\langle 220 \rangle$ 

<221> PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (22)$ 

<223> Xaa is Hyp



Xaa Leu Lys Cys Cys Ala  
20

<213> Conus purpurascens

<223> Xaa is Hyp

Lys Xaa His Arg Cys Cys  
20

<213> Conus magus

Pro Gln Arg Cys Cys Ala  
20

<213> Conus marmoreus

Lys Pro Ala Arg Cys Cys Gly Pro  
20

<213> Conus nobilis

Lys Asn Leu Lys Cys Cys Ser  
20

<213> Conus parius

Lys Pro Ala Arg Cys Cys Gly Pro  
20

<213> Conus parius

Pro Ala Arg Cys Cys Gly Pro  
20

<213> Conus radiatus

<223> Xaa is Hyp

Cys Lys Arg Asn Xaa Cys Cys Thr  
20

<213> Conus radiatus

<223> Xaa is Hyp

Arg Ser Lys Xaa Cys Cys Lys Ser  
20

<213>    Conus radiatus

Lys Pro Ala Arg Cys Cys Gly Pro  
20

<210> 515  
 <211> 23  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 515  
 Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
 20

<210> 516  
 <211> 21  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa is Hyp

<400> 516  
 His Gly Cys Cys Lys Gly Xaa Glu Gly Cys Ser Ser Arg Glu Cys Arg  
 1 5 10 15

Xaa Gln His Cys Cys  
 20

<210> 517  
 <211> 21  
 <212> PRT  
 <213> Conus tulipa

<400> 517  
 His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg Glu Cys Arg  
 1 5 10 15

Pro Gln His Cys Cys  
 20

<210> 518  
 <211> 23  
 <212> PRT  
 <213> Conus wittigi

<400> 518  
 Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro Ala Cys  
 1 5 10 15

Ile Arg His Gln Cys Cys Thr  
 20

<210> 519  
 <211> 17  
 <212> PRT  
 <213> Conus omaria

<400> 519  
 Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly Cys Thr Pro Cys Asp  
 1 5 10 15

Cys

<210> 520

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<211> 17
<212> PRT
<213> Conus omaria
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Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly Cys Thr Pro Cys Gly
1          5          10          15
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Cys

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